IN THE SPECIFICATION

Kindly enter the following paragraphs.

Page 1, insert the priority claim as a separate paragraph after the title:

This is a divisional of Appln. No. 09/545,002, filed April 6, 2000, allowed; which is a divisional of Appln. No. 08/969,125, filed November 12, 1997, now U.S. Patent No. 6,143,871; the entire contents of which are hereby incorporated by reference in this application.

Page 7, delete the third paragraph starting on line16 and replace it with:

For example, the extracellular region of the polypeptide having the sequence shown in Figure 1 (SEQ ID NO:8 and SEQ ID NO:9) could be used on its own as a soluble polypeptide capable of binding human IL-13 or human IL-4. Furthermore, one or more amino acid substitutions, insertions and/or deletions relative to said polypeptide could be made to provide other soluble polypeptides capable of binding human IL-13 or human IL-4. Indeed a skilled person could use protein binding studies to determine which part of said polypeptide is involved in binding human IL-13 and/or human IL-4. This could be done by scanning, directed or deletion mutagenesis, crosslinking with the ligands followed by protease digestion and sequencing, X-ray crystallography of the cytokine-receptor complex, epitope mapping of blocking antibodies, phage display libraries. Parts of the polypeptides having the sequence shown in Figure 1 which are not involved in binding could therefore be identified and could be omitted when producing other polypeptides within the scope of the present invention.

Page 22, insert before line 1 the new heading:

BRIEF DESCRIPTION OF THE DRAWINGS

Page 22, delete the second paragraph starting on line 4 and replace it with:

Figure 1 shows the nucleotide sequence (SEQ ID NO:8) and deduced amino acid sequence (SEQ ID NO:9) of the insert of the cDNA clone 3.1. The putative signal and

transmembrane region are indicated using bold [bolt] characters. The WSXWS (SEQ ID NO:2) motif is underlined. The GC rich region of the cDNA is underlined double (see Example 1).

Page 22, delete the fourth paragraph starting on line 16 and replace it with: Figures 3A-3C show [shows] the Northern blot analysis of IL-13Rα1 and IL-13Rα2 mRNA in primary human cells and cell lines (panel A), B cells and cell lines (panel B) and T cells and T cell clones (panel C). Total RNA (poly A^+ when specified in the figure) was isolated from the indicated cells. The Northern blot assay was performed with 2 µg RNA aliquots except for RNA isolated from peripheral T cell for which 1 µg aliquots were used. Peripheral T cells and JY were subjected to the indicated stimulation before RNA isolation. The membranes were stained with methylene blue (lower panel) and hybridized with the cDNA probes for IL-13Rα1 or IL-13Rα2. Autoradiography exposure time: IL-13Rα1, 24 h; IL-13Rα2, 7 days (see Examples 3, 4, 5).

Page 22, delete the fifth paragraph starting on line 28 and replace it with: Figures 4A-4C show [shows] radioligand affinity cross-linking of IL4 and IL13 to IL4Rα and IL13Rα1 transfectants. COS7 cells transiently transfected either with the cDNA of the human IL4Rα (A), the human IL13 Rα1 (B) or both (C) were detached and labeled with 0.5 nmol/L of [^{125}I]IL4 or 3 nmol/L of [^{125}I]IL13 as indicated. Displacement of the radioiodinated ligand was performed with a 1000 fold excess of unlabeled cytokine or with buffer (-) before cross-linking was performed using 2.5 mmol/L disuccinimidyl suberate. The lysates were analyzed under reducing conditions on a gradient (3-10%) SDS-PAGE, and exposed to X-ray films for 1-3 days. Net molecular masses of the receptors (R) were calculated by subtracting 19 kDa for bound IL4 or 15 kDa for bound IL13 (see Example 6).

Page 23, delete the second paragraph starting on line 10 and replace it with: Figures 5A-5C show [shows] binding of radiolabeled IL4 and IL13 to IL4Rα and IL13Rα1 transfectants. Receptor binding analysis of radiolabeled IL4 (▲) and IL13 ( )

was performed with COS7 cells transiently transfected with [[(A)]] the cDNA of either the human IL4Rα (full line) (panel A), the IL13Rα1 (dashed line) [[or]] (panel B) or cotransfected with both cDNAs (panel C). Data were analyzed with the computerized weighted least-square curve fitting software described by Porrelli *et al* (*Recept. Res.* **13**: 6 (1993)) [[7]] (see Example 7).

Page 24, delete the second paragraph starting on line 5 and replace it with:

Cloning of a human IL-13 R chain. To obtain a probe we searched the Gene Bank expressed sequence tag (EST) data base with the sequence of the extracellular protein domain of a known murine IL-13 receptor (IL-13 R) chain. (The cloning of said chain is disclosed in Hilton *et al*, *PNAS* 93:497 (1996)). The sequence of two ESTs (H57074 and H89334) with reading frames which encode peptides with a high degree of sequence identity to the murine IL-13 R chain were used to design PCR oligonucleotide primers. These primers were used to amplify a segment of the human IL-13 R cDNA from activated tonsilar B cell cDNA (see Materials and Methods). This human IL-13 R cDNA fragment was used to screen a λgt10 library of activated tonsilar B cell cDNA and to clone a human IL-13 R cDNA. Sequencing of the largest cDNA insert obtained from the screening revealed a 4 Kb mRNA sequence with an open reading frame encoding for a 427 amino acid polypeptide (Fig. [fig.] 1). The deduced polypeptide includes two hydrophobic regions likely to represent a signal peptide and a transmembrane domain. The transmembrane domain is followed by a 59 amino acid cytoplasmic region. Interestingly this region contains a YXXQ (SEQ ID NO:1) sequence motif which has been identified as a consensus for STAT binding (ref. 56). The extracellular domain includes the four cystein residues and WSXWS (SEQ ID NO:2) motif conserved among the type-I cytokine receptor superfamily (ref. 43).

Page 33, delete the first paragraph starting on line 2 and replace it with:

The Gene Bank EST data base was searched using the murine IL-13 R α extracytoplasmic domain protein sequence as query. Two EST with open reading frames with high degrees of amino acid identity were identified (EST H57074 and

H899334). The EST sequence was used to design the PCR primers CTGAGCTACATGAAGTGTTCTTGGCTCCCT (SEQ ID NO:3) and CAGAGTTTGTCATCCTCATAGCATAACTTA (SEQ ID NO:4) and the probe AATACCACTCCCGACACTAACTATACTCTC (SEQ ID NO:5).

Page 35, delete the second paragraph starting on line 14 and replace it with: We used either cDNA or cRNA probes for the detection [dectection] of IL-13 receptor α1 and α2 chain mRNA. IL-13 receptor α1 chain [^{32}P]-labelled cDNA probes were obtained by labelling the *Xmn*I-*Sca*I restriction fragment of the cDNA by random hexamer priming (ref. 49). To produce a cRNA probe specific for IL-13 receptor α1 chain the same fragment was recloned in the *Eco*RV site of pBluescript II SK and used for the transcription of a [^{32}P]-labelled probe (ref. 53). To produce probes specific for the IL-13 receptor α2 chain, the cDNA was amplified by PCR from the tonsilar B cell cDNA used previously for the cloning of the α1 chain cDNA, using the primers GGAGAAATGGCTTTCGTTTGCTTGGCTATC (SEQ ID NO:6) and TACCATGTCTCTTGATATGGAAAGTCTTCA (SEQ ID NO:7). The cDNA was cloned in the pCRII vector. cDNA probes were labelled with [^{32}P] by random hexamer priming (ref. 49). cRNA probes labelled with [^{32}P] were generated by transcribing the region in 3' of the cDNA insert *Eco*RV restriction site (ref. 53).